

SUPPLEMENTARY MATERIAL

SUPPLEMENTARY MATERIALS AND METHODS

Electrophoretic mobility shift assays (EMSA) were performed in 20 µl of 25 mM HEPES (pH7.8), 50 mM KCl, 10 mM MgCl₂, 1 mM DTT, 0.1 mg/ml BSA, and 0.1 µg/µl poly(dI-dC), 20 fmol of radioactively labeled double stranded DNA template containing the MTERF1 binding sequence (wt or with position 3241-3244 deleted) and increasing amounts of MTERF1 as indicated in the figure legends. The samples were incubated at room temperature for 20 min and then analyzed on a 6% non-denaturing PAGE.

LEGENDS TO SUPPLEMENTARY FIGURES

Figure S1. A electrophoretic mobility shift assay was used to investigate MTERF1 binding to a dsDNA oligonucleotide containing the wt MTERF1 binding site or a mutant derivative thereof.

Table S1. Primers used for ChIP analysis of TWINKLE binding

Name	Location in mtDNA	Sequence
1 Forward	2855-2878	GCT AAG ACT TCA CCA GTC AAA GCG
1 Reverse	2997-2974	TCC AAC ATC GAG GTC GTA AAC CCT
2 Forward	3012-3032	TGG TGC AGC CGC TAT TAA AGG
2 Reverse	3131-3151	TAG GCC TTA TTT CTC TTG TCC
3 Forward	3186-3206	TCT CAA CTT AGT ATT ATA CCC
3 Reverse	3292-3312	GGG TAT GTT GTT AAG AAG AGG
4 Forward	3230-3253	TGT TAA GAT GGC AGA GCC CGG TAA
4 Reverse	3356-3380	CGT TCG GTA AGC ATT AGG AAT GCC A
5 Forward	3355-3375	ATG GCA TTC CTA ATG CTT ACC
5 Reverse	3476-3496	CGG GTT TTA GGG GCT CTT TGG
6 Forward	3532-3555	ACC TTA GCT CTC ACC ATC GCT CTT
6 Reverse	3675-3698	CCG ATC AGG GCG TAG TTT GAG TTT
7 Forward	3704-3727	TGC GAG CAG TAG CCC AAA CAA TCT
7 Reverse	3833-3856	TTA TGG CCA AGG GTC ATG ATG GCA
8 Forward	3917-3940	AGT CCG AAC TAG TCT CAG GCT TCA
8 Reverse	4010-4033	GGA AGA TTG TAG TGG TGA GGG TGT

